

IN THE SPECIFICATION

Page 6, replace the paragraph starting on line 8 with the following:
Milk-clotting enzymes like ~~Fromase®~~ FROMASE® aspartic acid protease are also very well suited as auxiliary enzyme in the reduction or prevention of haze when used in combination with Endo-Pro. like ~~Fromase®~~ FROMASE® aspartic acid protease is well suited for this purpose since it does not affect LPT1 and therewith preserves the foam forming ability of the beer.

Page 6, replace the paragraph starting on line 12 with the following:
~~Fromase~~ FROMASE® aspartic acid protease is a commercial product ~~[[()]]~~ of DSM Food Specialities, ~~which was [()]]~~ obtained from Rhizomucor miehei that is used in cheese production. ~~Fromase~~ FROMASE® aspartic acid protease is a so-called aspartic protease (EC 3.4.23). These enzymes are characterised by very low pH optima and an outspoken preference for cleaving peptide bonds between bulky, hydrophobic amino acid residues such as Phe-Phe, Phe-Tyr and Leu-Tyr. Other aspartic acid proteases are pepsin, cathepsin and the various acid proteases from different fungi.

Page 17, replace the paragraph starting on line 24 with the following:
Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pair (HSPs) by identifying short words of length W in the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extensions for the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either

sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.